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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:17:09 ; Search time 138.5 Seconds
                                          (without alignments)
                                          545.655 Million cell updates/sec

Title: US-10-825-068-2
Perfect score: 907
Sequence: 1 CYLSRKLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   907   100.0   172 2   AAR54768   Aar54768 Sheep int
     2   907   100.0   172 2   AAR99397   Aar99397 Ovine tau
     3   907   100.0   172 2   AAW31698   Aaw31698 Mature ov
     4   907   100.0   172 2   AAW44110   Aaw44110 Mature ov
     5   907   100.0   172 5   ABB07588   Abb07588 Ovine int
     6   907   100.0   172 7   ADI17857   Adi17857 Mature ov
     7   907   100.0   172 8   ADM79177   Adm79177 Mature ov
     8   907   100.0   172 8   ADS13613   Ads13613 Sheep int

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:27:09 ; Search time 34 Seconds
                                            (without alignments)
                                            418.242 Million cell updates/sec

Title: US-10-825-068-2
Perfect score: 907
Sequence: 1 CYLSRKLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % | | | | |
| Result | | Query | | | | |
No.	Score	Match	Length	DB	ID	Description
1	907	100.0	172	1	US-08-438-753B-2	Sequence 2, Appli
2	907	100.0	172	1	US-08-443-883A-2	Sequence 2, Appli
3	907	100.0	172	1	US-08-631-328-2	Sequence 2, Appli
4	907	100.0	172	1	US-08-455-524B-2	Sequence 2, Appli
5	907	100.0	172	1	US-08-455-021B-2	Sequence 2, Appli
6	907	100.0	172	2	US-09-045-467-2	Sequence 2, Appli
7	907	100.0	172	2	US-08-954-395A-18	Sequence 18, Appl
8	907	100.0	172	2	US-08-616-904-2	Sequence 2, Appli
9	907	100.0	172	2	US-10-029-890-2	Sequence 2, Appli
10	900	99.2	172	2	US-09-599-413-2	Sequence 2, Appli
11	898	99.0	172	2	US-09-599-413-7	Sequence 7, Appli

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:28:04 ; Search time 115 Seconds
                                            (without alignments)
                                            624.927 Million cell updates/sec

Title: US-10-825-068-2
Perfect score: 907
Sequence: 1 CYLSRKLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
                 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   907   100.0   172   3   US-09-746-919-2   Sequence 2, Appli
     2   907   100.0   172   3   US-09-910-406C-2   Sequence 2, Appli
     3   907   100.0   172   4   US-10-029-890-2   Sequence 2, Appli
     4   907   100.0   172   4   US-10-346-269-2   Sequence 2, Appli
     5   907   100.0   172   4   US-10-346-269-3   Sequence 3, Appli
     6   907   100.0   172   4   US-10-694-247-2   Sequence 2, Appli
     7   907   100.0   172   4   US-10-683-214-1   Sequence 1, Appli
     8   907   100.0   172   4   US-10-794-495-2   Sequence 2, Appli
     9   907   100.0   172   4   US-10-719-472-2   Sequence 2, Appli
    10   907   100.0   172   5   US-10-825-068-2   Sequence 2, Appli
    11   907   100.0   172   5   US-10-884-741-2   Sequence 2, Appli

```
                       GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:          April  4, 2006, 18:29:20 ; Search time 15.5 Seconds
                                            (without alignments)
                                            337.807 Million cell updates/sec

Title:           US-10-825-068-2
Perfect score:   907
Sequence:        1 CYLSRKLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters:      180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA_New:*
                 1:  /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 2:  /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3:  /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4:  /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 5:  /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 6:  /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 7:  /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 8:  /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result           Query
   No.   Score  Match Length DB  ID                          Description
------------------------------------------------------------------------------
     1     907  100.0    172   7  US-11-177-010-2             Sequence 2, Appli
     2     907  100.0    172   7  US-11-112-369-1             Sequence 1, Appli
     3     899   99.1    172   7  US-11-177-010-4             Sequence 4, Appli
     4     899   99.1    172   7  US-11-112-369-2             Sequence 2, Appli
     5     473   52.1    172   6  US-10-519-390-11            Sequence 11, Appl
     6     473   52.1    194   6  US-10-936-447-20            Sequence 20, Appl
     7     473   52.1    757   6  US-10-936-447-8             Sequence 8, Appli
     8     440   48.5    166   7  US-11-132-722-49            Sequence 49, Appl
     9     440   48.5    166   7  US-11-176-830-187           Sequence 187, App
```

```
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OM protein - protein search, using sw model

Run on:         April  4, 2006, 18:22:20 ; Search time 24.5 Seconds
                                           (without alignments)
                                           675.481 Million cell updates/sec


Title:          US-10-825-068-2
Perfect score:  907
Sequence:       1 CYLSRKLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172


Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5


Searched:       283416 seqs, 96216763 residues


Total number of hits satisfying chosen parameters:      283416


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :      PIR_80:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
```

		% Query				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	897	98.9	195	2	JS0204	trophoblast interf
2	880	97.0	195	2	I47068	trophoblast protei
3	868	95.7	195	2	I47066	trophoblast protei
4	865	95.4	195	2	I47069	trophoblast protei
5	847	93.4	172	2	A61578	trophoblast protei
6	846	93.3	195	2	I46272	trophoblast interf
7	842	92.8	195	2	A61455	trophoblast protei
8	806	88.9	195	2	I47067	trophoblast protei
9	778	85.8	195	2	I47097	trophoblast protei
10	745	82.1	184	2	I47098	trophoblast protei
11	724	79.8	195	2	A39505	trophoblast interf
12	723	79.7	195	2	S23751	trophoblast interf
13	720	79.4	195	2	B39505	trophoblast protei

OM protein - protein search, using sw model

Run on: April 4, 2006, 18:17:34 ; Search time 145.5 Seconds
                                            (without alignments)
                                            834.027 Million cell updates/sec

Title: US-10-825-068-2
Perfect score: 907
Sequence: 1 CYLSRKLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   907 100.0   195   1   IFNT1_SHEEP   P56828 ovis aries
     2   900   99.2   195   1   IFNT2_SHEEP   P56829 ovis aries
     3   888   97.9   172   1   IFNT3_SHEEP   P56832 ovis aries
     4   881   97.1   195   1   IFNT4_SHEEP   Q28594 ovis aries
     5   880   97.0   195   1   IFNT7_SHEEP   Q08071 ovis aries
     6   877   96.7   195   1   IFNT5_SHEEP   Q28595 ovis aries
     7   868   95.7   195   1   IFNT9_SHEEP   Q08070 ovis aries
     8   865   95.4   195   1   IFNT8_SHEEP   Q08072 ovis aries
     9   846   93.3   195   1   IFNT_CAPHI   P28171 capra hircu
    10   842   92.8   195   1   IFNT6_SHEEP   Q29429 ovis aries
    11   830   91.5   195   2   Q6UZ49_CAPHI   Q6uz49 capra hircu
    12   830   91.5   195   2   Q6UZ50_CAPHI   Q6uz50 capra hircu
    13   816   90.0   172   2   Q6RFZ8_SHEEP   Q6rfz8 ovis aries
    14   806   88.9   195   1   IFNTA_SHEEP   Q08053 ovis aries
    15   804   88.6   195   2   Q6UZ47_CAPHI   Q6uz47 capra hircu

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:17:09 ; Search time 138.5 Seconds
                                           (without alignments)
                                           545.655 Million cell updates/sec

Title: US-10-825-068-3
Perfect score: 907
Sequence: 1 CYLSERLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result   Query
  No.   Score Match Length DB ID   Description
----
      1   907 100.0   172 5 ABB07589   Abb07589 Recombina
      2   907 100.0   172 8 ADM79178   Adm79178 Mature ov
      3   907 100.0   172 8 ADS13614   Ads13614 Recombina
      4   907 100.0   172 9 AEA18013   Aea18013 Recombina
      5   907 100.0   172 9 AEA39574   Aea39574 Recombina
      6   901   99.3   195 2 AAR24941   Aar24941 Sequence
      7   901   99.3   195 2 AAR24945   Aar24945 Sequence
      8   899   99.1   172 2 AAR54768   Aar54768 Sheep int

```
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OM protein - protein search, using sw model

Run on:           April  4, 2006, 18:27:09 ; Search time 34 Seconds
                                             (without alignments)
                                             418.242 Million cell updates/sec


Title:            US-10-825-068-3
Perfect score:    907
Sequence:         1 CYLSERLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172


Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5


Searched:         572060 seqs, 82675679 residues


Total number of hits satisfying chosen parameters:      572060


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :        Issued_Patents_AA:*
                  1:  /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                  2:  /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                  3:  /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                  4:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  5:  /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                  6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*


      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
```

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	899	99.1	172	1	US-08-438-753B-2	Sequence 2, Appli
2	899	99.1	172	1	US-08-443-883A-2	Sequence 2, Appli
3	899	99.1	172	1	US-08-631-328-2	Sequence 2, Appli
4	899	99.1	172	1	US-08-455-524B-2	Sequence 2, Appli
5	899	99.1	172	1	US-08-455-021B-2	Sequence 2, Appli
6	899	99.1	172	2	US-09-045-467-2	Sequence 2, Appli
7	899	99.1	172	2	US-08-954-395A-18	Sequence 18, Appl
8	899	99.1	172	2	US-08-616-904-2	Sequence 2, Appli
9	899	99.1	172	2	US-10-029-890-2	Sequence 2, Appli
10	894	98.6	172	2	US-09-599-413-18	Sequence 18, Appl
11	892	98.3	172	2	US-09-599-413-2	Sequence 2, Appli

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:28:04 ; Search time 115 Seconds
                                           (without alignments)
                                           624.927 Million cell updates/sec

Title: US-10-825-068-3
Perfect score: 907
Sequence: 1 CYLSERLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
                 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                             SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   907   100.0   172   3   US-09-910-406C-4   Sequence 4, Appli
     2   907   100.0   172   4   US-10-683-214-2   Sequence 2, Appli
     3   907   100.0   172   4   US-10-719-472-3   Sequence 3, Appli
     4   907   100.0   172   5   US-10-825-068-3   Sequence 3, Appli
     5   907   100.0   172   5   US-10-884-741-3   Sequence 3, Appli
     6   907   100.0   172   5   US-10-825-382-3   Sequence 3, Appli
     7   907   100.0   172   5   US-10-825-457-3   Sequence 3, Appli
     8   907   100.0   172   5   US-10-824-710-3   Sequence 3, Appli
     9   907   100.0   172   5   US-10-991-653-3   Sequence 3, Appli
    10   907   100.0   172   6   US-11-078-608-3   Sequence 3, Appli
    11   907   100.0   172   6   US-11-040-706-3   Sequence 3, Appli

```
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OM protein - protein search, using sw model

Run on:          April  4, 2006, 18:29:20 ; Search time 15.5 Seconds
                                            (without alignments)
                                            337.807 Million cell updates/sec

Title:           US-10-825-068-3
Perfect score:   907
Sequence:        1 CYLSERLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters:       180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA_New:*
                 1:  /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 2:  /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3:  /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4:  /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 5:  /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 6:  /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 7:  /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 8:  /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                       %
Result              Query
   No.    Score    Match Length DB  ID                         Description
-------------------------------------------------------------------------------
      1     907   100.0    172   7  US-11-177-010-4        Sequence 4, Appli
      2     907   100.0    172   7  US-11-112-369-2        Sequence 2, Appli
      3     899    99.1    172   7  US-11-177-010-2        Sequence 2, Appli
      4     899    99.1    172   7  US-11-112-369-1        Sequence 1, Appli
      5     474    52.3    172   6  US-10-519-390-11       Sequence 11, Appl
      6     474    52.3    194   6  US-10-936-447-20       Sequence 20, Appl
      7     474    52.3    757   6  US-10-936-447-8        Sequence 8, Appli
      8     441    48.6    166   7  US-11-132-722-49       Sequence 49, Appl
      9     441    48.6    166   7  US-11-176-830-187      Sequence 187, App
```

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:22:20 ; Search time 24.5 Seconds
                                            (without alignments)
                                            675.481 Million cell updates/sec

Title: US-10-825-068-3
Perfect score: 907
Sequence: 1 CYLSERLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                 %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   901   99.3   195 2   JS0204   trophoblast interf
     2   878   96.8   195 2   I47068   trophoblast protei
     3   872   96.1   195 2   I47066   trophoblast protei
     4   869   95.8   195 2   I47069   trophoblast protei
     5   844   93.1   195 2   I46272   trophoblast interf
     6   839   92.5   172 2   A61578   trophoblast protei
     7   834   92.0   195 2   A61455   trophoblast protei
     8   810   89.3   195 2   I47067   trophoblast protei
     9   782   86.2   195 2   I47097   trophoblast protei
    10   749   82.6   184 2   I47098   trophoblast protei
    11   729   80.4   195 2   A39505   trophoblast interf
    12   727   80.2   195 2   S23751   trophoblast interf
    13   724   79.8   195 2   B39505   trophoblast protei

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:17:34 ; Search time 145.5 Seconds
                                            (without alignments)
                                    834.027 Million cell updates/sec

Title: US-10-825-068-3
Perfect score: 907
Sequence: 1 CYLSERLMLDARENLKLLDR..........TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
     1   904   99.7   195   1   IFNT2_SHEEP   P56829 ovis aries
     2   899   99.1   195   1   IFNT1_SHEEP   P56828 ovis aries
     3   896   98.8   172   1   IFNT3_SHEEP   P56832 ovis aries
     4   885   97.6   195   1   IFNT4_SHEEP   Q28594 ovis aries
     5   881   97.1   195   1   IFNT5_SHEEP   Q28595 ovis aries
     6   878   96.8   195   1   IFNT7_SHEEP   Q08071 ovis aries
     7   872   96.1   195   1   IFNT9_SHEEP   Q08070 ovis aries
     8   869   95.8   195   1   IFNT8_SHEEP   Q08072 ovis aries
     9   844   93.1   195   1   IFNT_CAPHI   P28171 capra hircu
    10   834   92.0   195   1   IFNT6_SHEEP   Q29429 ovis aries
    11   828   91.3   195   2   Q6UZ49_CAPHI   Q6uz49 capra hircu
    12   828   91.3   195   2   Q6UZ50_CAPHI   Q6uz50 capra hircu
    13   820   90.4   172   2   Q6RFZ8_SHEEP   Q6rfz8 ovis aries
    14   810   89.3   195   1   IFNTA_SHEEP   Q08053 ovis aries
    15   802   88.4   195   2   Q6UZ47_CAPHI   Q6uz47 capra hircu

RESULT 3
AAW31698
ID   AAW31698 standard; protein; 172 AA.
XX
AC   AAW31698;
XX
DT   14-APR-1998 (first entry)
XX
DE   Mature ovine interferon-tau (OvIFNtau) protein.
XX
KW   Interferon-tau; ovine; human; auto immune disease; treatment; toxicity;
KW   IFN tau; multiple sclerosis; diabetes mellitus; asthma; allergy; cancer.
XX
OS   Ovis aries.
XX
PN   WO9733607-A1.
XX
PD   18-SEP-1997.
XX
PF   12-MAR-1997;   97WO-US003794.
XX
PR   15-MAR-1996;   96US-00616904.
XX
PA   (UYFL) UNIV FLORIDA.
XX
PI   Soos JM, Schiffenbauer J, Johnson HM;
XX
DR   WPI; 1997-470642/43.
DR   N-PSDB; AAV02288.
XX
PT   Oral administration of interferon-tau for treatment of auto-immune
PT   disease - avoids toxicity of interferon alpha and generates fewer
PT   specific antibodies than injection.
XX
PS   Claim 5; Page 31; 48pp; English.
XX
CC   This is a mature ovine interferon-tau (OvIFNtau) protein. The ovine and
CC   the human interferon-tau (IFN tau) can be used in the treatment of
CC   mammalian diseases responsive to IFN tau. The new feature in the
CC   treatment is that IFN tau is administered orally. The method is used to
CC   treat immune, particularly autoimmune disease, specifically multiple
CC   sclerosis (a preferred application, reducing both severity and frequency
CC   of relapses), type I diabetes mellitus, lupus erythematosus, amyotrophic
CC   lateral sclerosis, Crohn's disease, rheumatoid arthritis, stomatitis,
CC   asthma, allergies and psoriasis, particularly in humans or dogs. IFN tau
CC   is also useful for treating cancer (e.g. hairy cell leukaemia, Kaposi's
CC   sarcoma and multiple myeloma), cell proliferation and viral diseases
CC   (hepatitis, human immunodeficiency virus etc., including prevention of
CC   maternal transmission). It is also used for increasing fertility in
CC   female mammals (increasing life time of the corpus luteum). Oral
CC   administration is as effective as injection but is more convenient and
CC   generates a lower level of anti-IFN tau antibodies. Use of IFN tau avoids
CC   the toxicity associated with use of IFN alpha
XX
SQ   Sequence 172 AA;

      Query Match   100.0%; Score 907; DB 2; Length 172;

```
Best Local Similarity   100.0%;  Pred. No. 1.2e-92;
   Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 CYLSRKLMLDARENLKLLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEM 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 CYLSRKLMLDARENLKLLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEM 60


Qy       61 LQQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPIVTV 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 LQQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPIVTV 120


Qy      121 KKYFQGIYDYLQEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTKMGGDLNSP 172
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KKYFQGIYDYLQEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTKMGGDLNSP 172
```